U.S. Appln. No.: 10/802,055

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the

application:

LISTING OF CLAIMS:

1. (currently amended): A method for the detection of an base sequence of interest in a

sample-DNA-or-RNA polynucleotide comprising-consisting essentially of the steps of:

(1) contacting a-the sample DNA or RNA polynucleotide with to at least one kind of

probe DNAs or RNAspolynucleotides in an aqueous solution to form a hybridization complex;

(2) isolating the hybridization complex;

(3) dissociating the hybridization complex to recover the probe DNAs or

RNAspolynucleotides; and

(4) identifying the said probe DNA or RNA polynucleotides to detect anthe base sequence

of interest in the sample DNA or RNApolynucleotide.

2. (currently amended): The method according to claim 1, wherein the hybridization is

carried out in such a manner that any none of the sample DNA or RNA polynucleotide and or the

probe DNAs or RNAs is notpolynucleotides are immobilized.

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3. (currently amended): The method according to claim 1 or 2, wherein plural kinds of probe DNAs or RNAspolynucleotides are used to detect plural base sequences of interest.

- **4.** (currently amended): The method according to any of claims 1 to 3 or 2, wherein the probe DNAs or RNAspolynucleotides are labeled with fluorescent substance.
- 5. (currently amended): The method according to any of-claims 1 to 4or 2, wherein the probe DNAs or RNAspolynucleotides are identified by means of hybridization with a polynucleotide chain complementary chain DNA thereofthereto.
- 6. (currently amended): The method according to claim 5, wherein the <u>polynucleotide</u> chains complementary to the probe polynucleotides chain DNAs or RNAs- are immobilized.
- 7. (currently amended): The method according to claim 6, wherein the immobilized polynucleotide chain complementary to the probe polynucleotides chain DNAs or RNA are in a the form of a DNA or RNA chip.
- **8.** (new): The method according to claim 1 or 2, wherein plural kinds of probe polynucleotides are used to detect plural, non-contiguous base sequences of interest.